

FIG 1

5' 11 20 29 38 47 56
 GGC GGA GGC GGA GGC GGA GGG CGA GGG GCG GGG AGC GCC GCC TGG AGC GCG GCA

 65 74 83 92 101 110
 GGT CAT ATT GAA CAT TCC AGA TAC CTA TCA TTA CTC GAT GCT GTT GAT AAC AGC

 119 128 137 146 155 164
 AAG ATG GCT TTG AAC TCA GGG TCA CCA CCA GCT ATT GGA CCT TAC TAT GAA AAC

 M A L N S G S P P A I G P Y Y E N

 173 182 191 200 209 218
 CAT GGA TAC CAA CCG GAA AAC CCC TAT CCC GCA CAG CCC ACT GTG GTC CCC ACT

 H G Y Q P E N P Y P A Q P T V V P T

 227 236 245 254 263 272
 GTC TAC GAG GTG CAT CCG GCT CAG TAC TAC CCG TCC CCC GTG CCC CAG TAC GCC

 V Y E V H P A Q Y Y P S P V P Q Y A

 281 290 299 308 317 326
 CCG AGG GTC CTG ACG CAG GCT TCC AAC CCC GTC GTC TGC ACG CAG CCC AAA TCC

 P R V L T Q A S N P V V C T Q P K S

 335 344 353 362 371 380
 CCA TCC GGG ACA GTG TGC ACC TCA AAG ACT AAG AAA GCA CTG TGC ATC ACC TTG

 P S G T V C T S K T K K A L C I T L

 389 398 407 416 425 434
 ACC CTG GGG ACC TTC CTC GTG GGA GCT GCG CTG GCC GCT GGC CTA CTC TGG AAG

 T L G T F L V G A A L A A G L L W K

 443 452 461 470 479 488
 TTC ATG GGC AGC AAG TGC TCC AAC TCT GGG ATA GAG TGC GAC TCC TCA GGT ACC

 F M G S K C S N S G I E C D S S G T

 497 506 515 524 533 542
 TGC ATC AAC CCC TCT AAC TGG TGT GAT GGC GTG TCA CAC TGC CCC GGC GGG GAG

 C I N P S N W C D G V S H C P G G E

 551 560 569 578 587 596
 GAC GAG AAT CGG TGT GTT CGC CTC TAC GGA CCA AAC TTC ATC CTT CAG GTG TAC

 D E N R C V R L Y G P N F I L Q V Y

 605 614 623 632 641 650
 TCA TCT CAG AGG AAG TCC TGG CAC CCT GTG TGC CAA GAC GAC TGG AAC GAG AAC

 S S Q R K S W H P V C Q D D W N E N

 659 668 677 686 695 704
 TAC GGG CGG GCG GCC TGC AGG GAC ATG GGC TAT AAG AAT AAT TTT TAC TCT AGC

 Y G R A A C R D M G Y K N N F Y S S

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1415	1424	1433	1442	1451	1460
GGG AAC GTC GAT TCT TGC CAG GGT GAC AGT GGA GGG CCT CTC GTC ACT TCG AAG					
-----	-----	-----	-----	-----	-----
G N V D S C Q G D S G G P L V T S K					
1469	1478	1487	1496	1505	1514
AAC AAT ATC TGG TGG CTG ATA GGG GAT ACA AGC TGG GGT TCT GGC TGT GCC AAA					
-----	-----	-----	-----	-----	-----
N N I W W L I G D T S W G S G C A K					
1523	1532	1541	1550	1559	1568
GCT TAC AGA CCA GGA GTG TAC GGG AAT GTG ATG GTA TTC ACG GAC TGG ATT TAT					
-----	-----	-----	-----	-----	-----
A Y R P G V Y G N V M V F T D W I Y					
1577	1586	1595	1604	1613	1622
CGA CAA ATG AGG GCA GAC GGC TAA TCC ACA TGG TCT TCG TCC TTG ACG TCG TTT					
-----	-----	-----	-----	-----	-----
R Q M R A D G *					
1631	1640	1649	1658	1667	1676
TAC AAG AAA ACA ATG GGG CTG GTT TTG CTT CCC CGT GCA TGA TTT ACT CTT AGA					
-----	-----	-----	-----	-----	-----
1685	1694	1703	1712	1721	1730
GAT GAT TCA GAG GTC ACT TCA TTT TTA TTA AAC AGT GAA CTT GTC TGG CAA AAA					
-----	-----	-----	-----	-----	-----
1739					
AAA AAA AAA A 3'					

002120" 5525F960

FIG 2

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1 gtcattattga acattccaga tacctatcat tactcgatgc tgttgataac agcaagatgg
61 ctttgaactc agggtcacca ccagctattg gaccttacta tgaaaacccat ggataccaac
121 cggaaaaccc ctatcccgca cagcccactg tgggtcccccac tgtctacgag gtgcatcccg
181 ctcagtacta cccgtccccc gtgcccaggt acgccccgag ggtcctgacg caggcttcca
241 accccgtcgt ctgcacgcag cccaaatccc catccgggac agtgtgcacc tcaaagacta
301 agaaagcact gtgcatcacc ttgaccttgg ggaccttccct cgtgggagct gcgctggccg
361 ctggcctact ctggaagtgc atgggcagca agtgctccaa ctctgggata gagtgcgact
421 cctcagggtac ctgcatcaac cctctaaact ggtgtgatgg cgtgtcacac tgccccggcg
481 gggaggacga gaatcggtgt gttcgctctc acggaccaa cttcatcctt cagatgtact
541 catctcagag gaagtcctgg caccctgtgt gccaaagacga ctggaacgag aactacgggc
601 gggcgccctg cagggacatg ggctataaga ataattttta ctctagccaa ggaatagtg
661 atgacagcgg atccaccagc tttatgaaac tgaacacaag tgccggcaat gtcgatatct
721 ataaaaaact gtaccacagt gatgcctggt cttcaaaaagc agtgggtttct ttacgctgtt
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901 gaggtcccat catcaccccc gagtggatcg tgacagccgc cactgctgtg gaaaaacctc
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1081 agaacaatga cattgcgctg atgaagctgc agaagcctct gactttcaac gacctagtga
1141 aaccagtgtg tctgccaac ccaggcattg tgctgcagcc agaacagctc tgctggattt
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1261 tgcttctcat tgagacacag agatgcaaca gcagatatgt ctatgacaac ctgatcacac
1321 cagccatgat ctgtgccggc ttctgcagg ggaacgtcga ttcttgccag ggtgacagt
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1861 tgagcatgga gctgtcactt ctgagctgct ggatgacttg agatgaaaaa ggagagacat
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1981 tccccagcct acttcacaag gggattttgc tgatgggttc ttagagcctt agcagcctg
2041 gatggtggcc agaaataaag ggaccagccc ttcattgggtg gtgacgtggt agtcacttgt
2101 aagggaagca gaaacatttt tgttcttatg gggtgagaat atagacagt cccttggtgc
2161 gaggaagca attgaaaagg aacttgccct gagcactcct ggtgcaggtc tccacctgca
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2341 atgtcggcct cttcaggcct gatagtcatt ggaaattgag gtccatgggg gaaatcaagg
2401 atgctcagtt taagggtacac tgtttccatg ttatgtttct acacattgat ggtggtgacc
2461 ctgagttcaa agccatctt

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ORF AMINO ACID SEQUENCE

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MALNSGSPPAIGPYYNHGYQPENPYPAQPTVVPTVYEVHPAQYYPSVPVQYAPRVLTQASNPVVCTQPKSPSGTV
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GPNFILQMYSSQRKSWHPVCQDDWNENYGRAACRDMGYKNNFYSSQGI VDDSGSTSFMKLNLSAGNVDIYKKLYHS
DACSSKAVVSLRCLACGVNLNSSRQSRIVGGESALPGAWPWQVSLHVQNVHVCGGSIITPEWIVTAHCVEKPLNN
PWHWTAFAGILRQSFMYGAGYQVQKVI SHPNYDSKTKNNDIALMKLQKPLTFNDLVKPVCLPNPGMMLQPEQLCW
ISGWGATEEKGKTSEVLNAKVLIIETQRCNSRYVDNLITPAMICAGFLQGNVDSQGDSSGGLVTSNNNIWWLI
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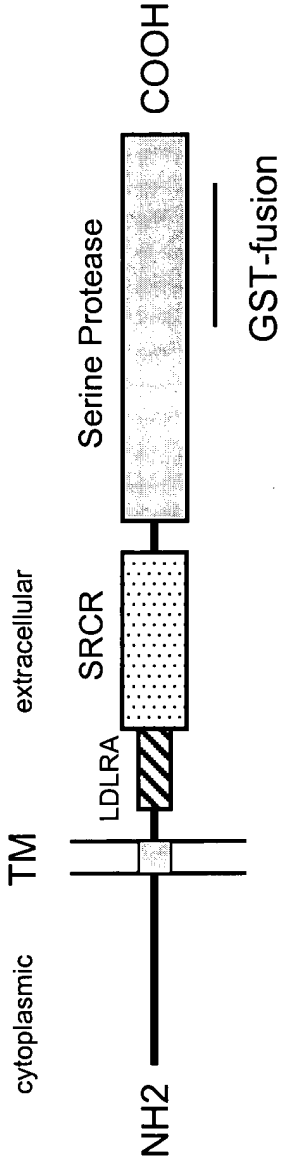
CAA	GGA	ATA	GTG	GAT	GAC	AGC	GGA	TCC	ACC	AGC	TTT	ATG	AAA	CTG	AAC	ACA	AGT
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Q	G	I	V	D	D	S	G	S	T	S	F	M	K	L	N	T	S
GCC	GGC	AAT	GTC	GAT	ATC	TAT	AAA	AAA	CTG	TAC	CAC	AGT	GAT	GCC	TGT	TCT	TCA
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A	G	N	V	D	I	Y	K	K	L	Y	H	S	D	A	C	S	S
AAA	GCA	GTG	GTT	TCT	TTA	CGC	TGT	ATA	GCC	TGC	GGG	GTC	AAC	TTG	AAC	TCA	AGC
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K	A	V	V	S	L	R	C	I	A	C	G	V	N	L	N	S	S
CGC	CAG	AGC	AGG	ATT	GTG	GGC	GGC	GAG	AGC	GCG	CTC	CCG	GGG	GCC	TGG	CCC	TGG
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R	Q	S	R	I	V	G	G	E	S	A	L	P	G	A	W	P	W
CAG	GTC	AGC	CTG	CAC	GTC	CAG	AAC	GTC	CAC	GTG	TGC	GGA	GGC	TCC	ATC	ATC	ACC
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Q	V	S	L	H	V	Q	N	V	H	V	C	G	G	S	I	I	T
CCC	GAG	TGG	ATC	GTG	ACA	GCC	GCC	CAC	TGC	GTG	GAA	AAA	CCT	CTT	AAC	AAT	CCA
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P	E	W	I	V	T	A	A	H	C	V	E	K	P	L	N	N	P
TGG	CAT	TGG	ACG	GCA	TTT	GCG	GGG	ATT	TTG	AGA	CAA	TCT	TTC	ATG	TTC	TAT	GGA
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W	H	W	T	A	F	A	G	I	L	R	Q	S	F	M	F	Y	G
GCC	GGA	TAC	CAA	GTA	GAA	AAA	GTG	ATT	TCT	CAT	CCA	AAT	TAT	GAC	TCC	AAG	ACC
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A	G	Y	Q	V	E	K	V	I	S	H	P	N	Y	D	S	K	T
AAG	AAC	AAT	GAC	ATT	GCG	CTG	ATG	AAG	CTG	CAG	AAG	CCT	CTG	ACT	TTC	AAC	GAC
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K	N	N	D	I	A	L	M	K	L	Q	K	P	L	T	F	N	D
CTA	GTG	AAA	CCA	GTG	TGT	CTG	CCC	AAC	CCA	GGC	ATG	ATG	CTG	CAG	CCA	GAA	CAG
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L	V	K	P	V	C	L	P	N	P	G	M	M	L	Q	P	E	Q
CTC	TGC	TGG	ATT	TCC	GGG	TGG	GGG	GCC	ACC	GAG	GAG	AAA	GGG	AAG	ACC	TCA	GAA
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L	C	W	I	S	G	W	G	A	T	E	E	K	G	K	T	S	E
GTG	CTG	AAC	GCT	GCC	AAG	GTG	CTT	CTC	ATT	GAG	ACA	CAG	AGA	TGC	AAC	AGC	AGA
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V	L	N	A	A	K	V	L	L	I	E	T	Q	R	C	N	S	R
TAT	GTC	TAT	GAC	AAC	CTG	ATC	ACA	CCA	GCC	ATG	ATC	TGT	GCC	GGC	TTC	CTG	CAG
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Y	V	Y	D	N	L	I	T	P	A	M	I	C	A	G	F	L	Q

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FIG 3A

1	15 16	30 31	45 46	60 61	75 76	90	
	GTCT	MALNSGPPAIGPY ENHGYQENPYPAQ	TVPVTVYEVHQAQY	PSVPQYAPRVLTOA	SNPVVCTQPKSPSGT	VCTSKTKKALCITLT	90
	TMPRSS2	MALNSGPPAIGPY ENHGYQENPYPAQ	TVPVTVYEVHQAQY	PSVPQYAPRVLTOA	SNPVVCTQPKSPSGT	VCTSKTKKALCITLT	90
	91	105 106	120 121	135 136	150 151	165 166	180
	GTCT	LGTFVLGAALAAAGLL WKFMGSKCSNSGIEC	DSSGTCINPSNWC	DG VSHCPGGEDENRCVR	LYGNFILQ	VYSSQR	KSWHPVCQDDWNENY
	TMPRSS2	LGTFVLGAALAAAGLL WKFMGSKCSNSGIEC	DSSGTCINPSNWC	DG VSHCPGGEDENRCVR	LYGNFILQ	VYSSQR	KSWHPVCQDDWNENY
	181	195 196	210 211	225 226	240 241	255 256	270
	GTCT	GRAACRDMGYKNNFY SSQGIIVDDSGSTFSM	KLNTSAGNVDIYKKL	YHSDACSSKAVVSLR	CLACGVNLN	SSRQSR	IVGESALPGAWPWQ
	TMPRSS2	GRAACRDMGYKNNFY SSQGIIVDDSGSTFSM	KLNTSAGNVDIYKKL	YHSDACSSKAVVSLR	CLACGVNLN	SSRQSR	IVGESALPGAWPWQ
	271	285 286	300 301	315 316	330 331	345 346	360
	GTCT	VSLHVQNVHVCGGSI ITPEWIVTAAHCVEK	PLNPNPWHWTA	FAGIL RQSFMYGAGYQV	QK VISHPNYDS	TKKNND	IALMKLQKPLTFNDL
	TMPRSS2	VSLHVQNVHVCGGSI ITPEWIVTAAHCVEK	PLNPNPWHWTA	FAGIL RQSFMYGAGYQV	QK VISHPNYDS	TKKNND	IALMKLQKPLTFNDL
	361	375 376	390 391	405 406	420 421	435 436	450
	GTCT	VKPVCLPNPGMMLQP EQLCWISGWGATEEK	GKTSEVLNAAKVLLI	ETQRCNSRYVYDNL	LI TPAMICAGFLQGNVD	SCQGD	SGGPLVTSNN
	TMPRSS2	VKPVCLPNPGMMLQP EQLCWISGWGATEEK	GKTSEVLNAAKVLLI	ETQRCNSRYVYDNL	LI TPAMICAGFLQGNVD	SCQGD	SGGPLVTSNN
	451	465 466	480 481				
	GTCT	NIWWLIGTWSGSGC AKAYRPGVYGNVMVF	TDWIYRQM	ADG			
	TMPRSS2	NIWWLIGTWSGSGC AKAYRPGVYGNVMVF	TDWIYRQM	ADG			

FIG 3B



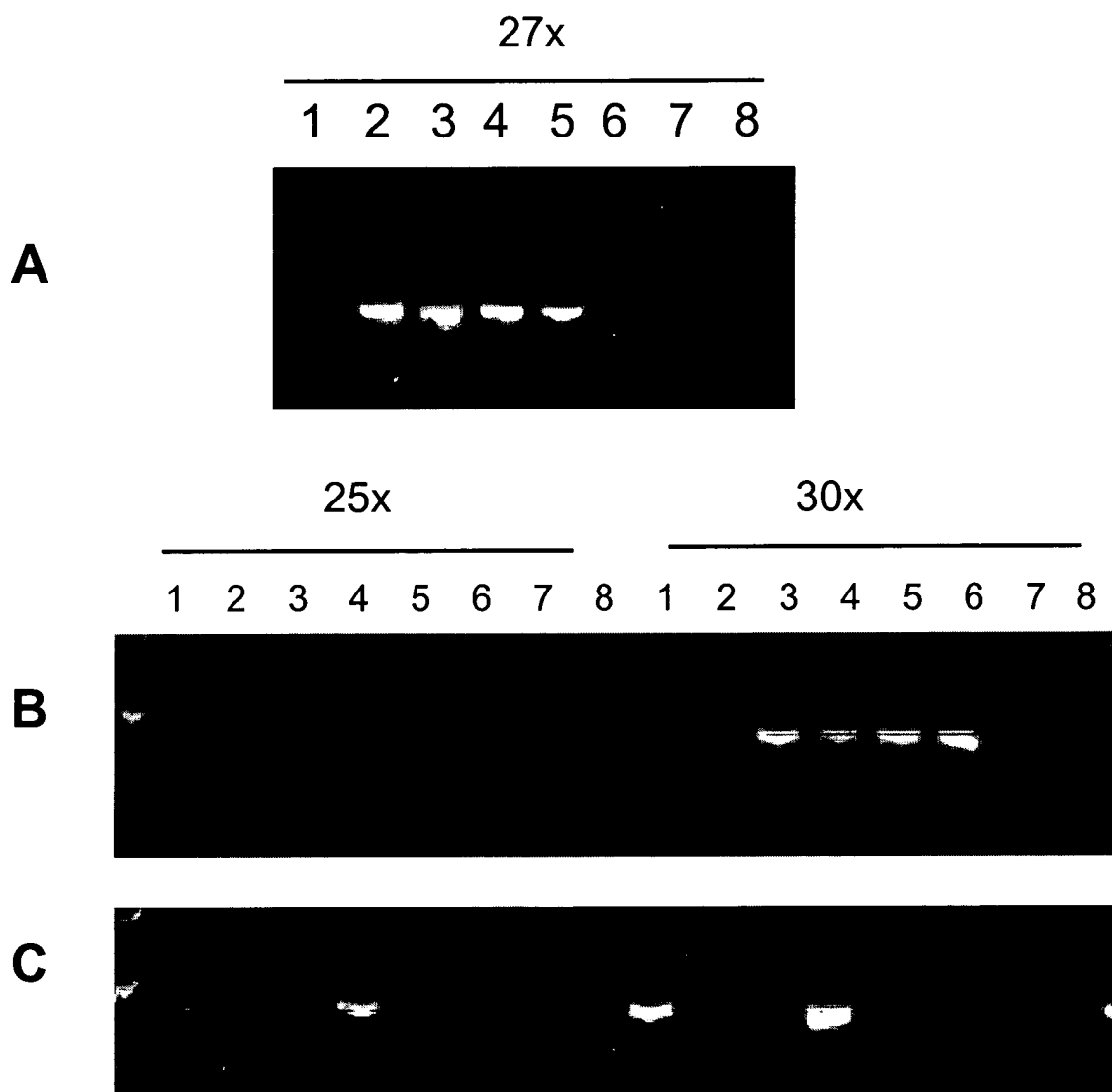
Cytoplasmic domain: a.a. 1-84
Protease domain: a.a. 255-492
SRCR domain: a.a. 149-242
LDLRA domain: a.a. 113-148
TM domain: a.a. 84-106
GST-fusion: a.a. 362-440

FIG 4

GATCTTCCTGCTGAGTCCTTTCCAGGGGCCAATTTTGGATGAGCATGGAGCTGTCACCTCTCAGCTGCTGGATGAC
TTGAGATGAAAAAGGAGAGACATGGAAAGGGAGACAGCCAGGTGGCACCTGCAGCGGCTGCCCTCTGGGGCCACTT
GGTAGTGTCCCCAGCCTACCTCTCCACAAGGGGATTTGCTGATGGGTTCCTTANAGCCTTAGCAGCCCTGGATGGT
GGCCAGAAATAAAGGGACCAGCCCTTCATGGGTGGTGACGTGGTANTCACTTGTAAAGGGGAACAGAAACATTTTG
TTCTTATGGGGTGAGAATATAGACAGTGCCCTTGGTGCGAGGGAAGCAATTGAAAAGGAACTTGCCCTGAGCACTC
CTGGTGCA

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FIG. 5



A

1. Brain
2. Prostate
3. LAPC-4 AD
4. LAPC-4 AI
5. LAPC-9 AD
6. HeLa
7. Murine cDNA
8. Neg. control

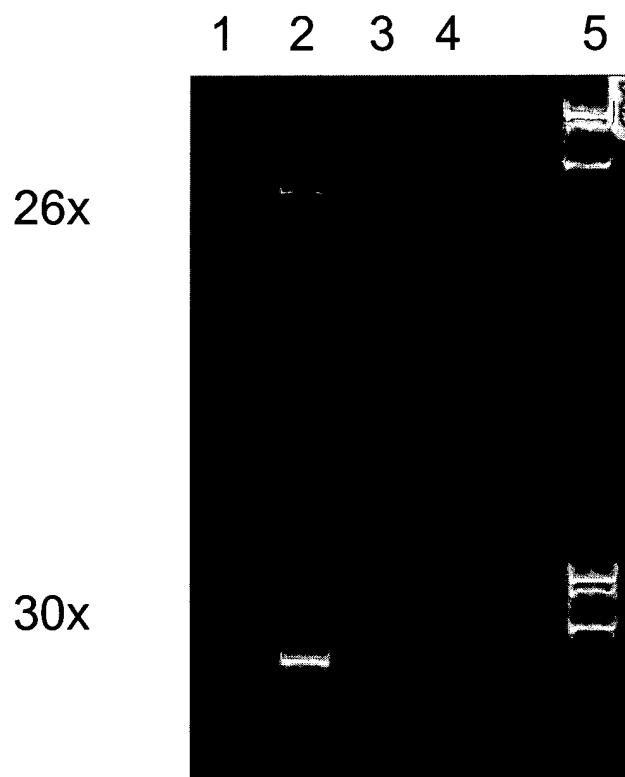
B

1. Brain
2. Heart
3. Kidney
4. Liver
5. Lung
6. Pancreas
7. Placenta
8. Skeletal Muscle

C

1. Colon
2. Ovary
3. Leukocytes
4. Prostate
5. Small Intestine
6. Spleen
7. Testis
8. Thymus

FIG 5D



- Prostate tumor pool
- Bladder tumor pool
- HeLa
- H₂O
- Markers

FIG. 6

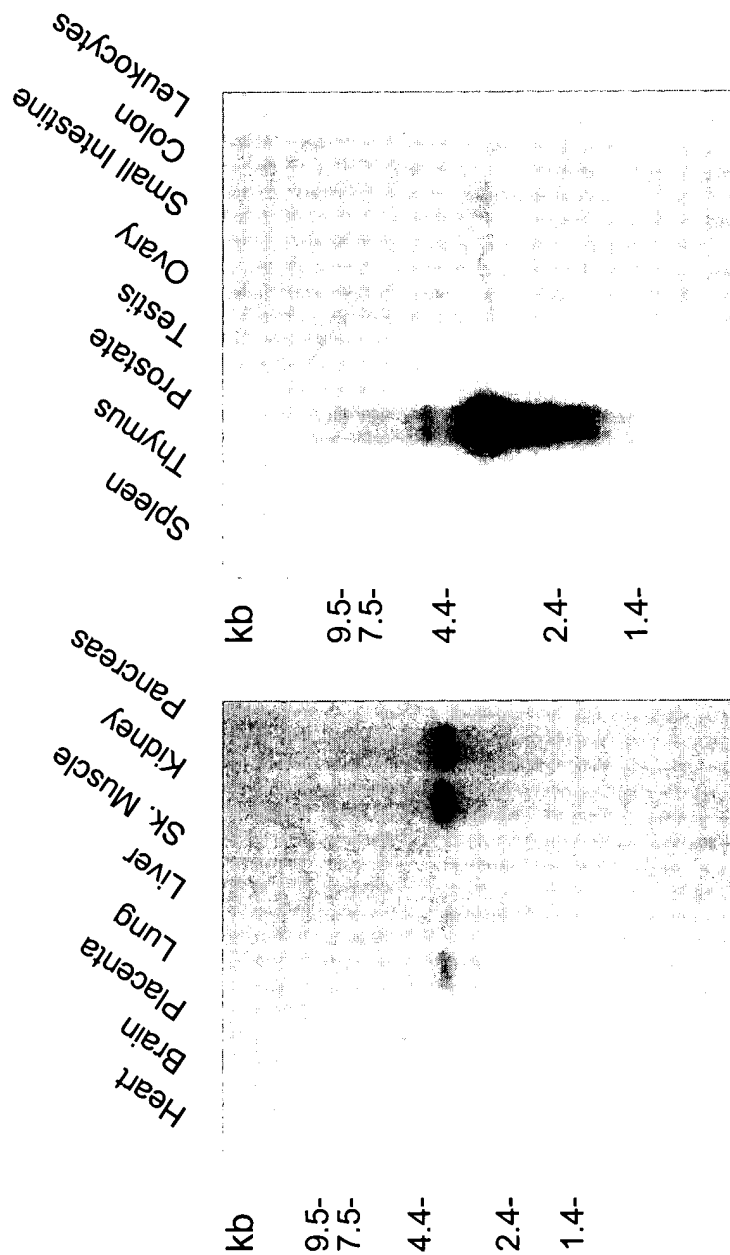


FIG. 7

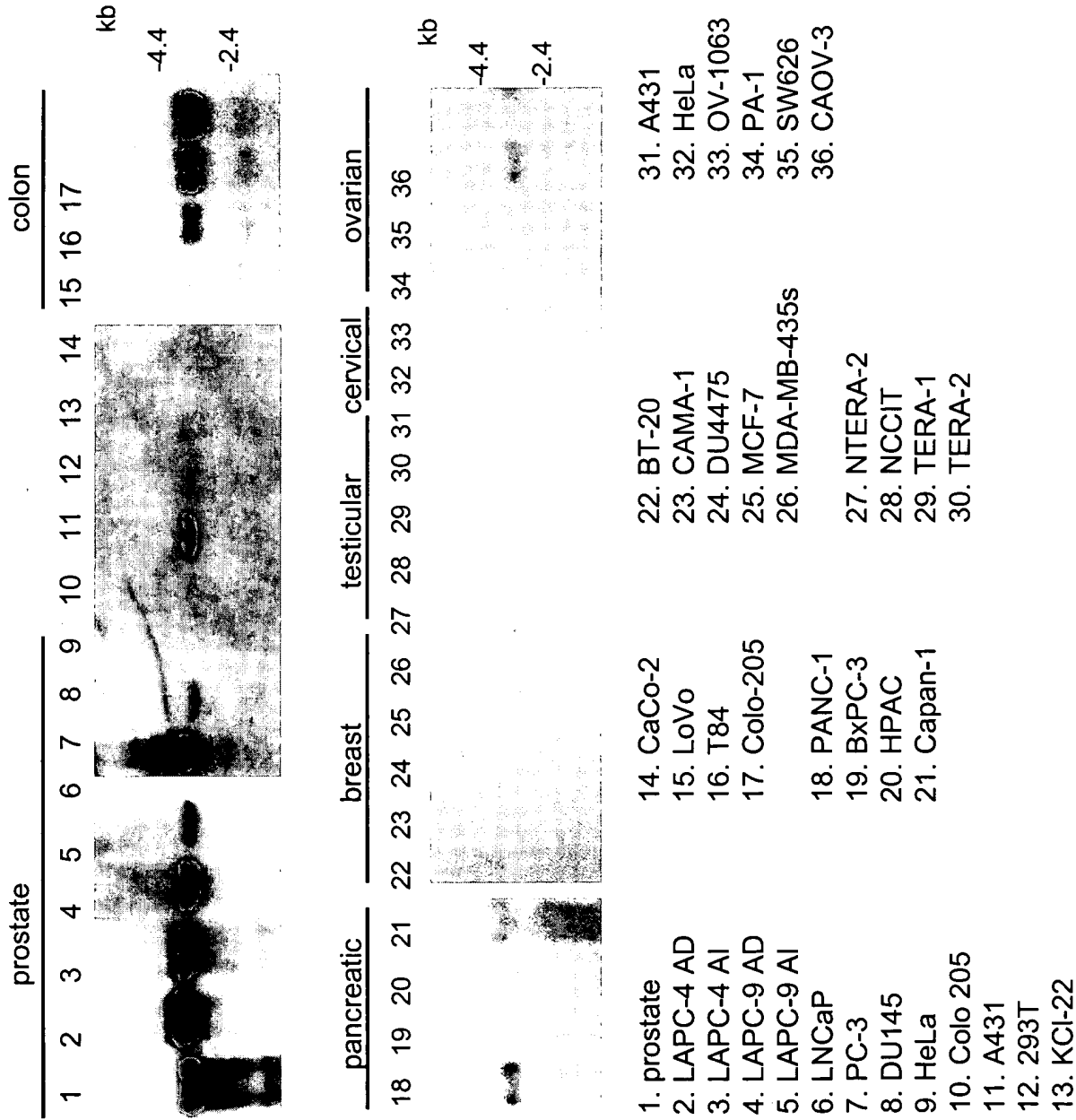


FIG. 8

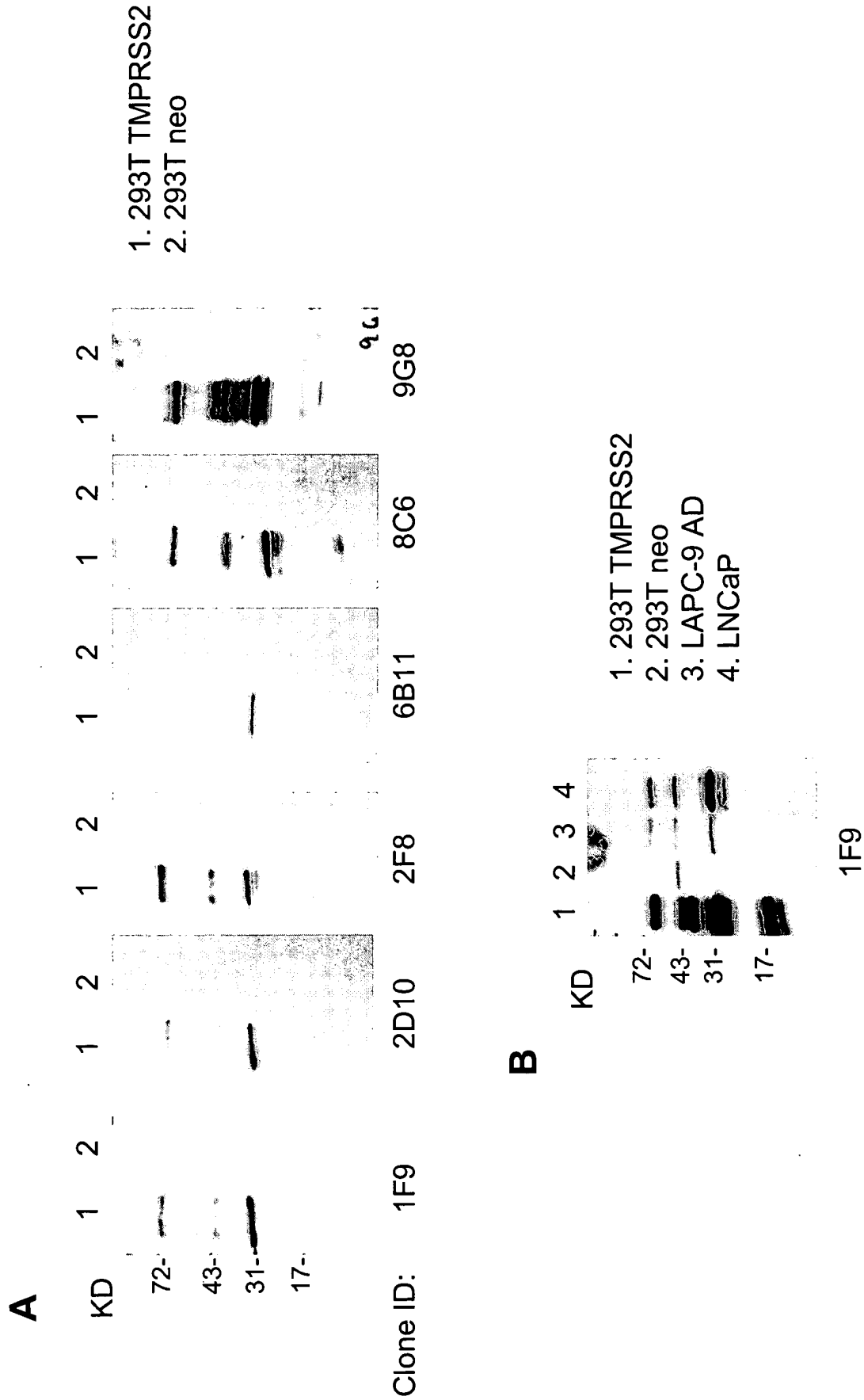
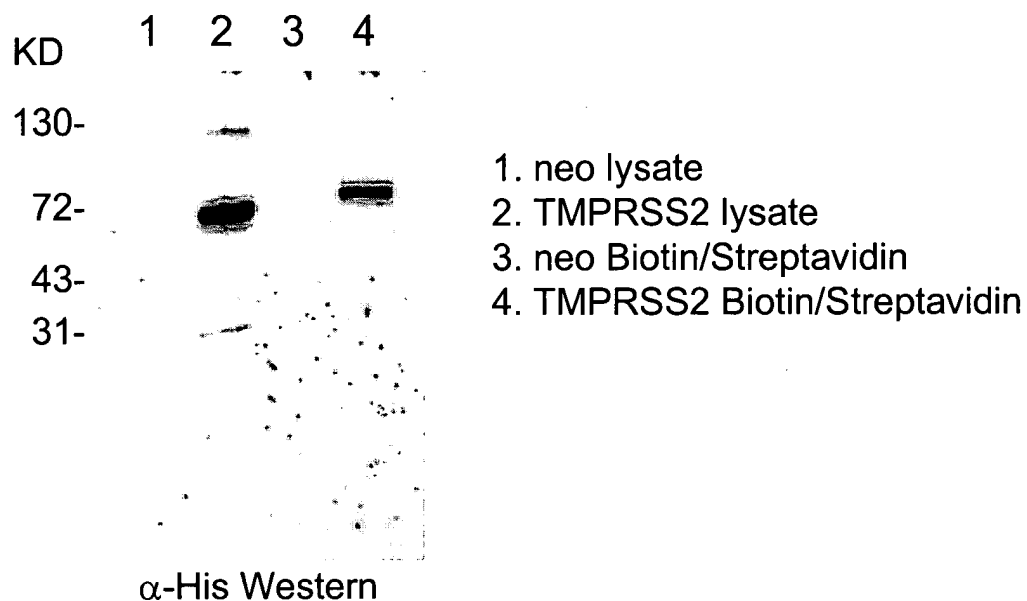


FIG. 9

A. In transfected 293T cells:



B. In prostate cancer cells:

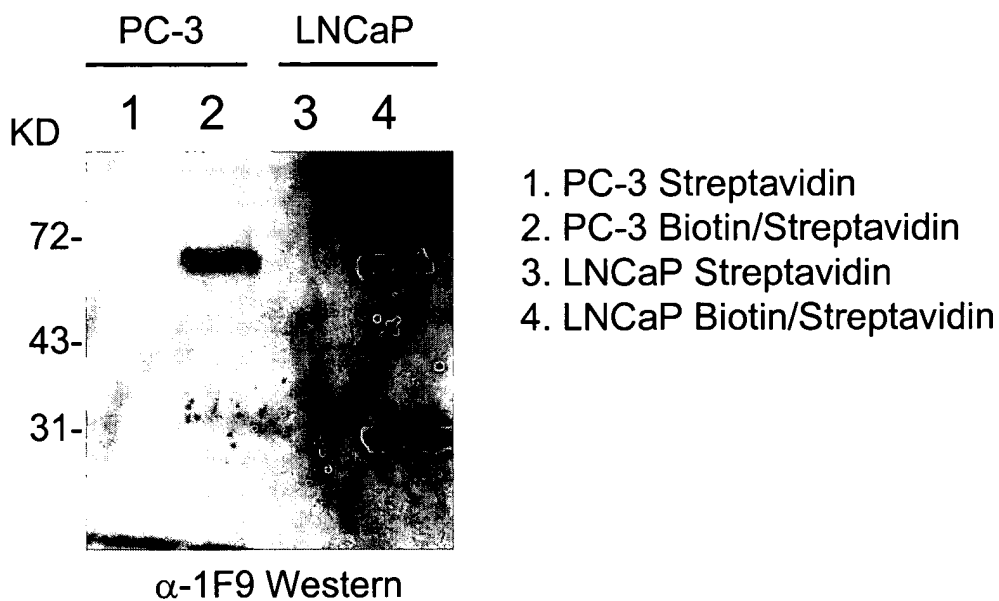


FIG. 10

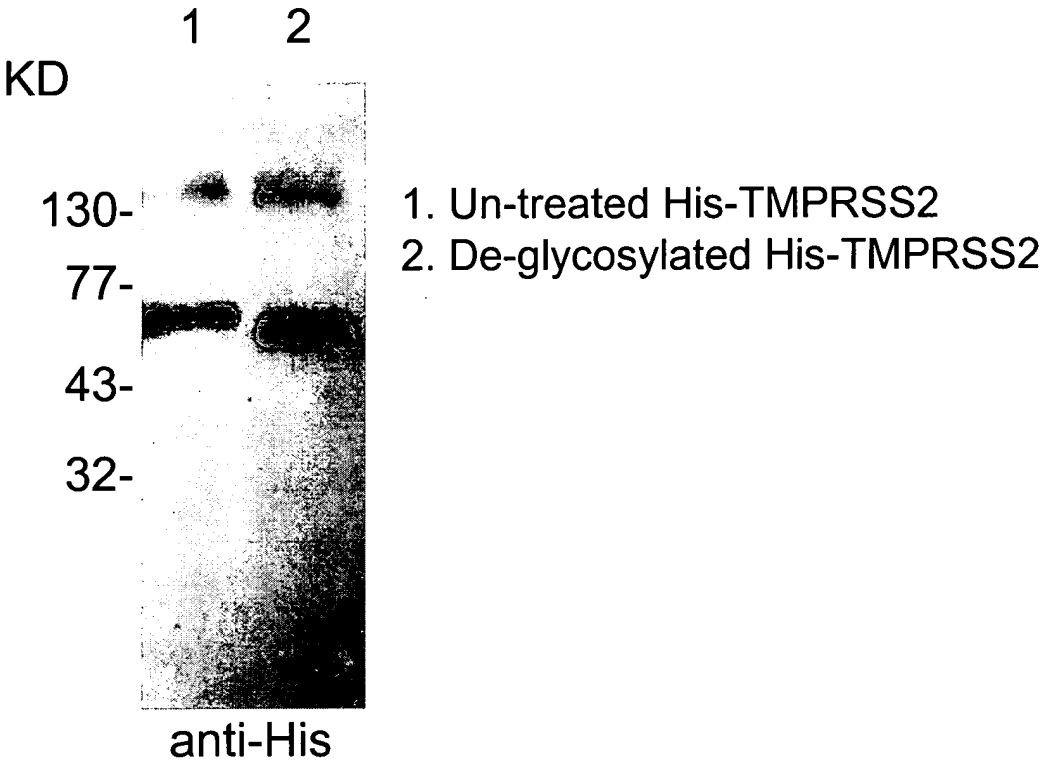
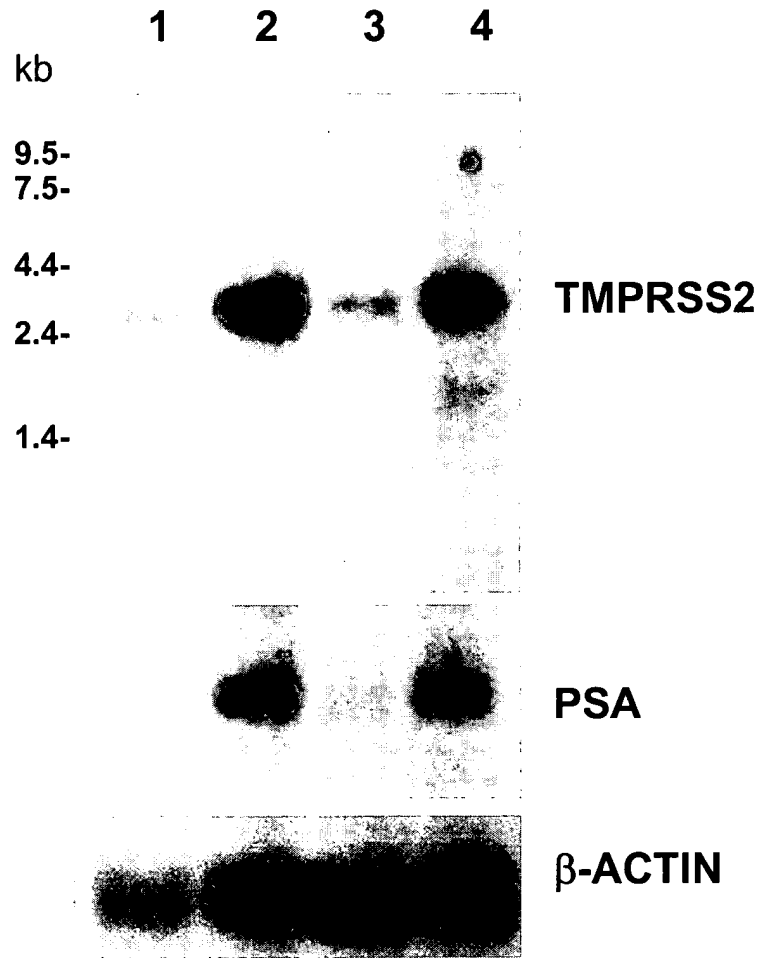


FIG. 11



Panel:

1. LNCaP androgen-deprived 1 week
2. LNCaP FBS
3. LNCaP androgen-deprived 24 hrs + mock 9 hrs
4. LNCaP androgen deprived 24 hrs + Mib 9hrs

0679

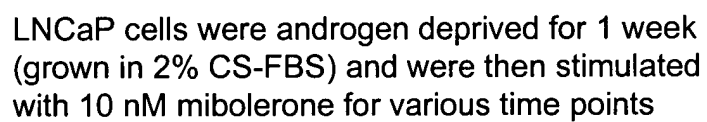
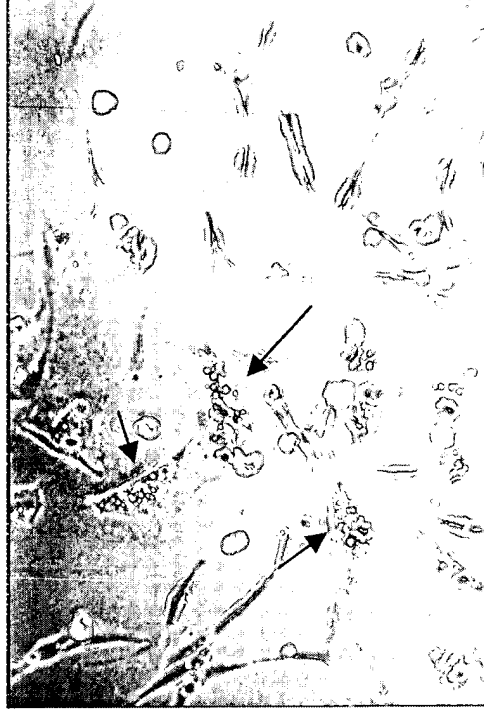


FIG. 13



NIH 3T3
neo



NIH 3T3
TMPRSS2

FIG 14

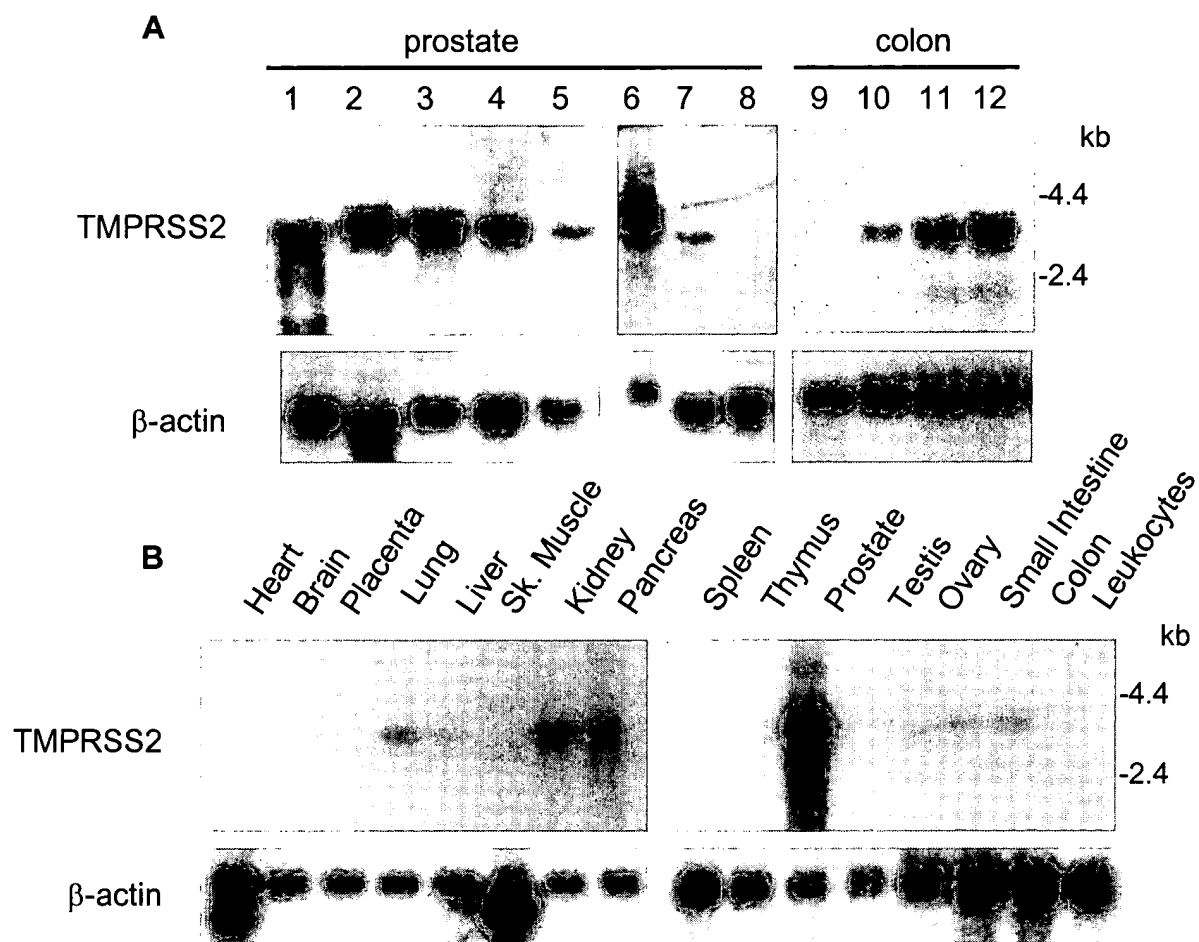


FIG 15

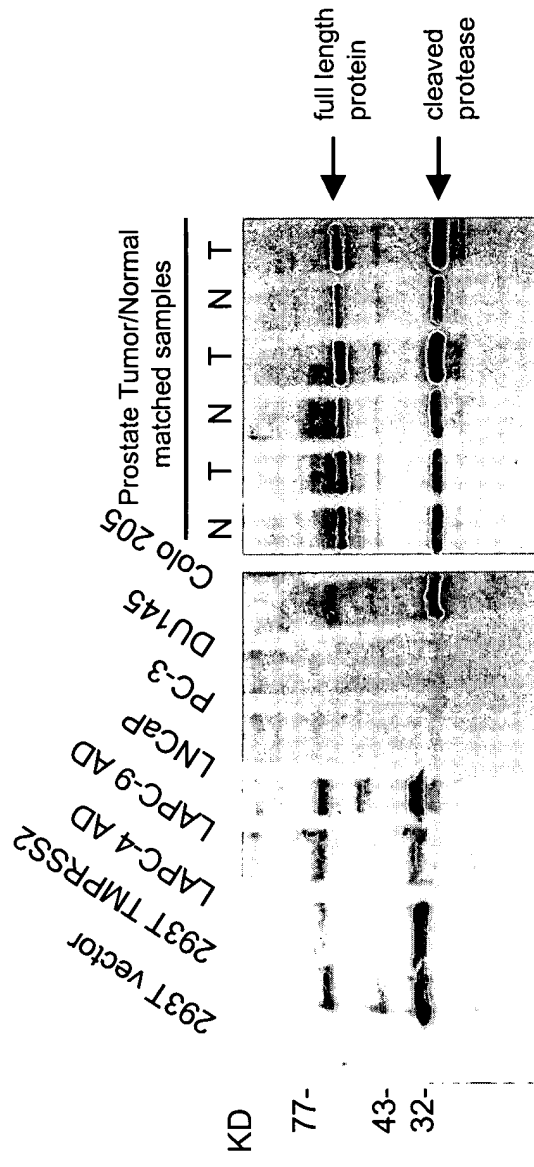
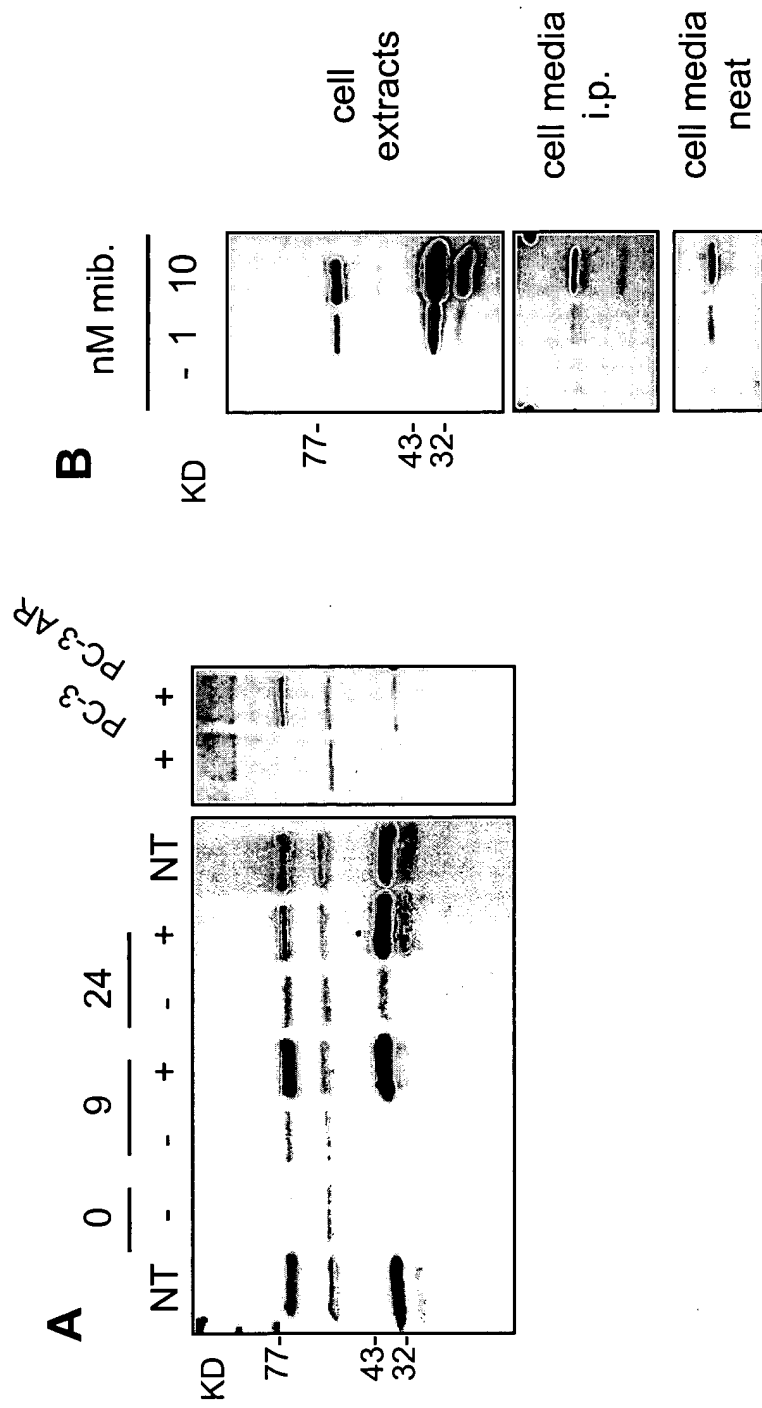


FIG 16



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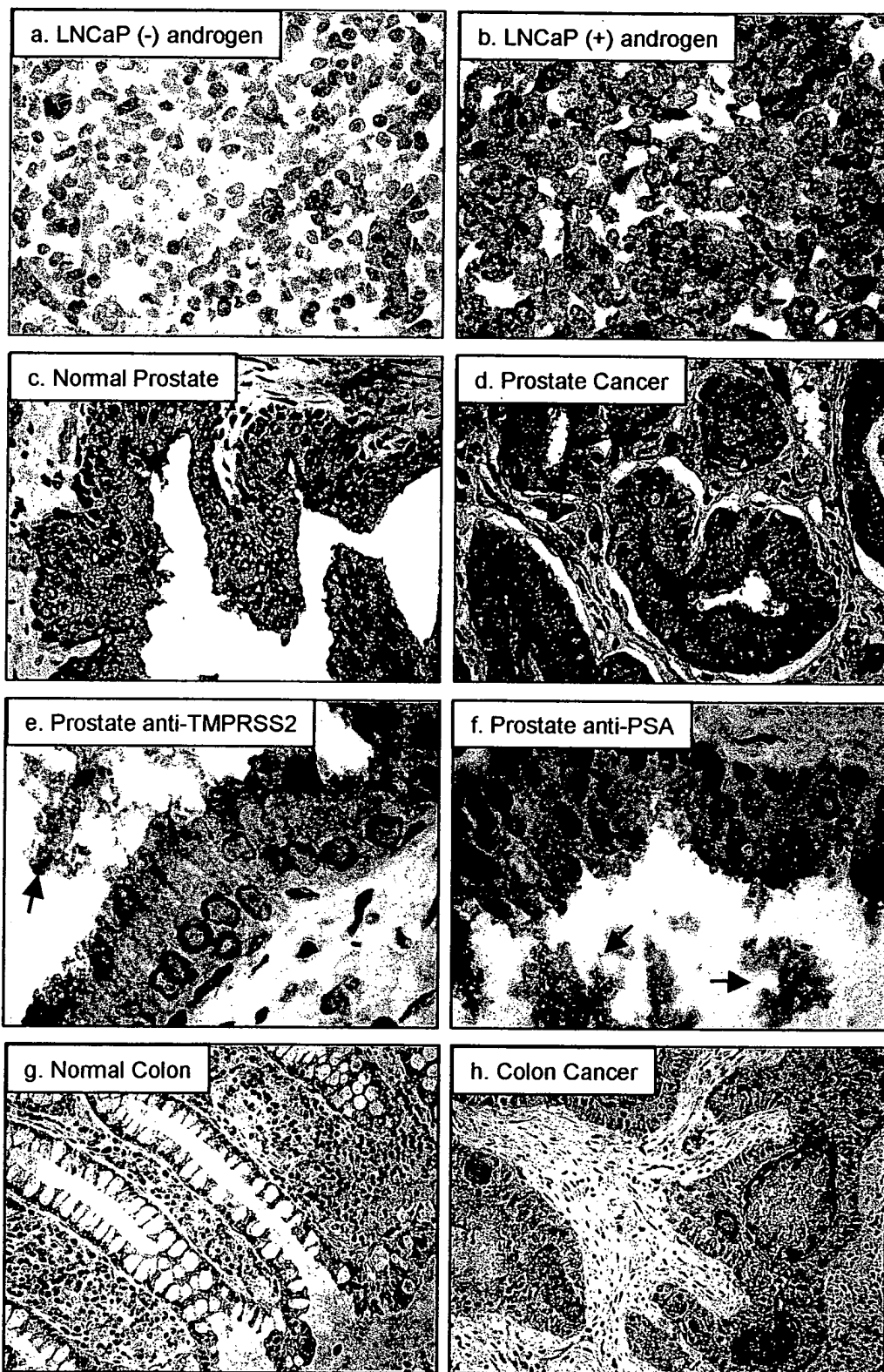


FIG 17

FIG 18

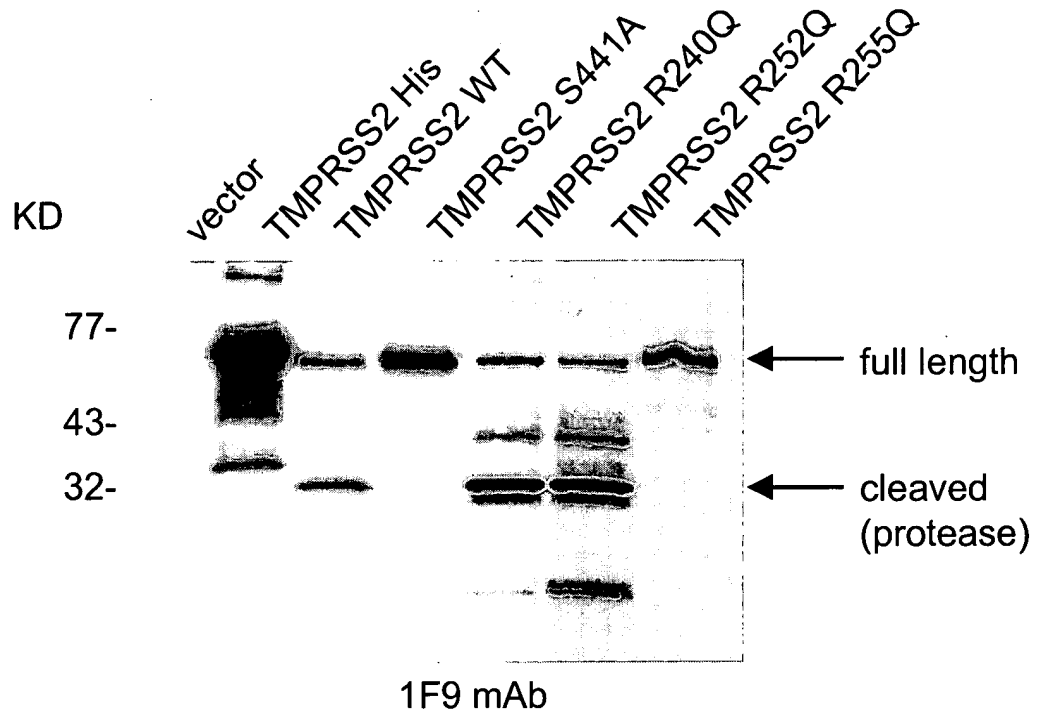


FIG 19

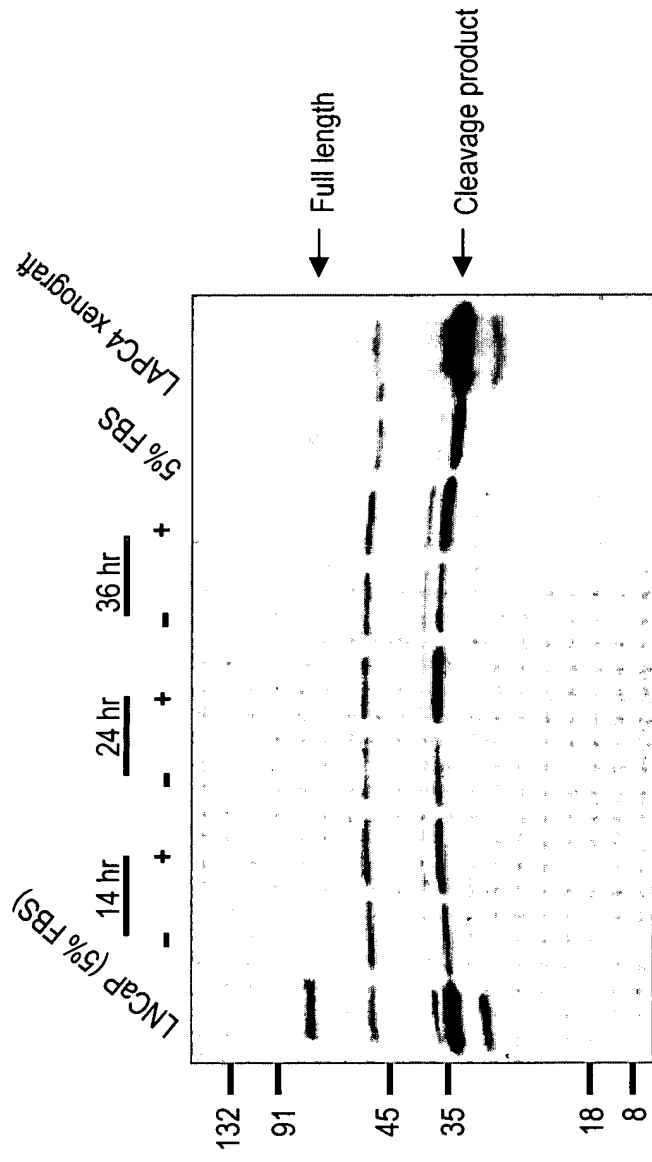
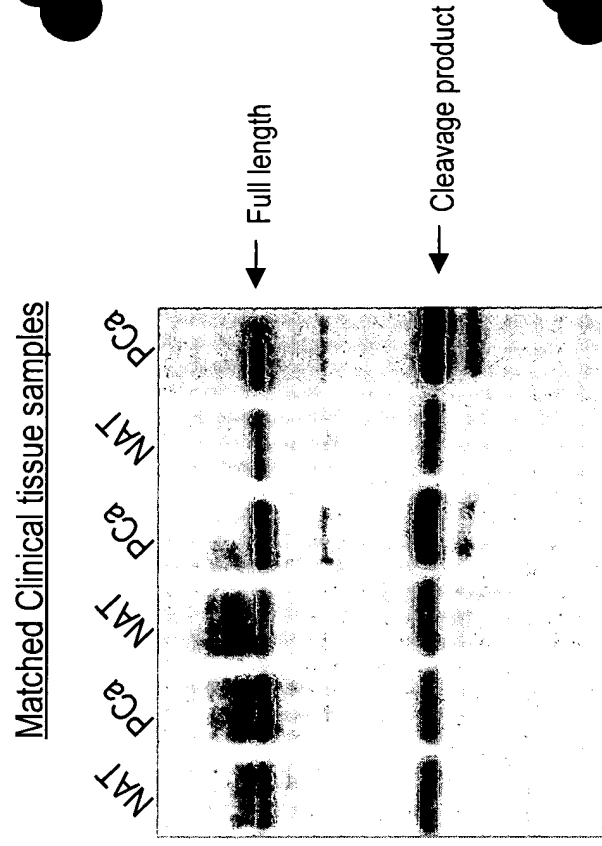
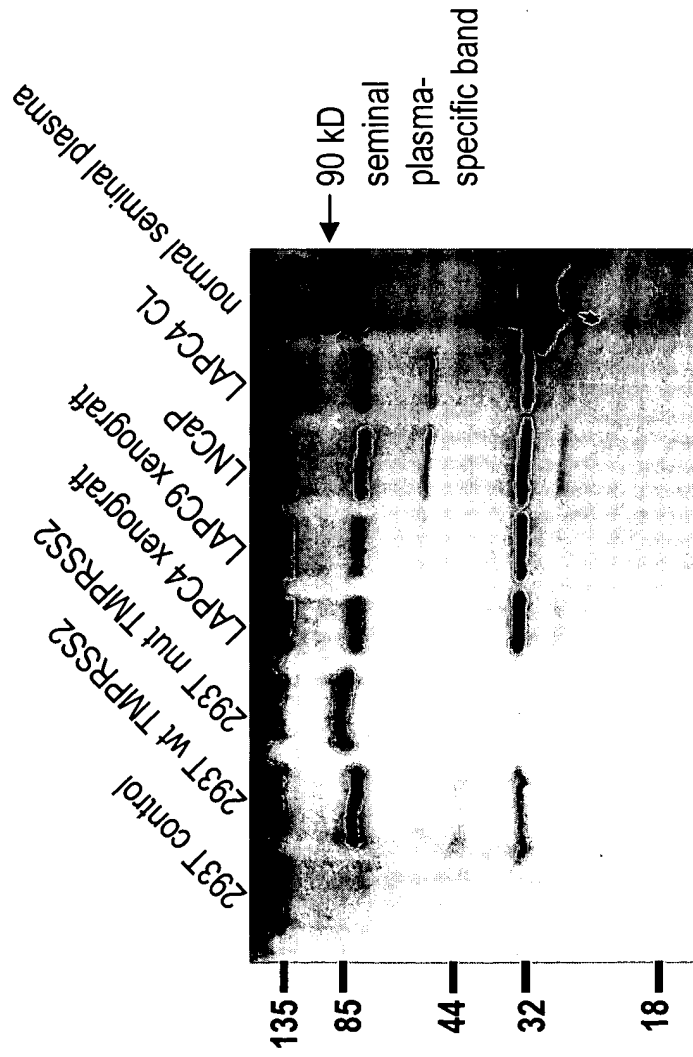


FIG 20



NAT: normal adjacent tissue
PCa: prostate cancer tissue

FIG 21

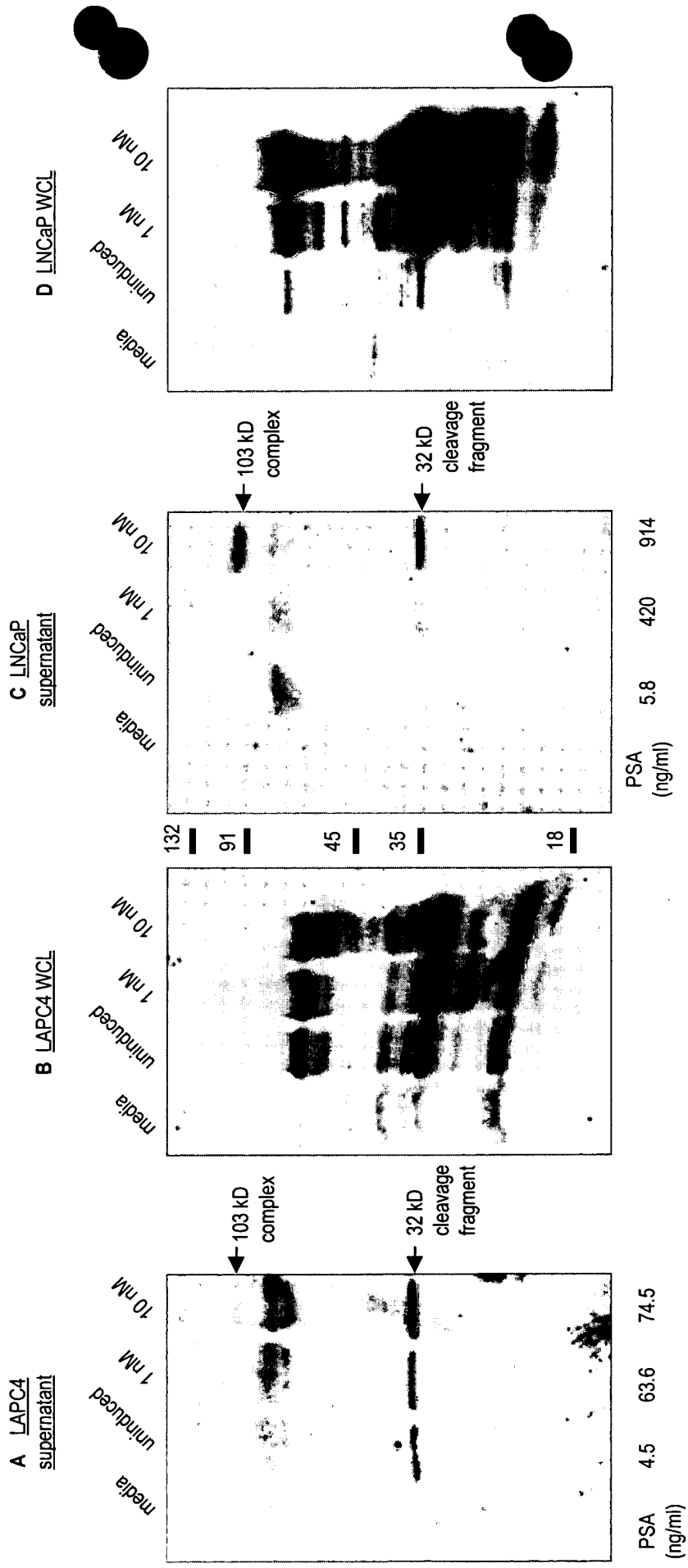


FIG 22

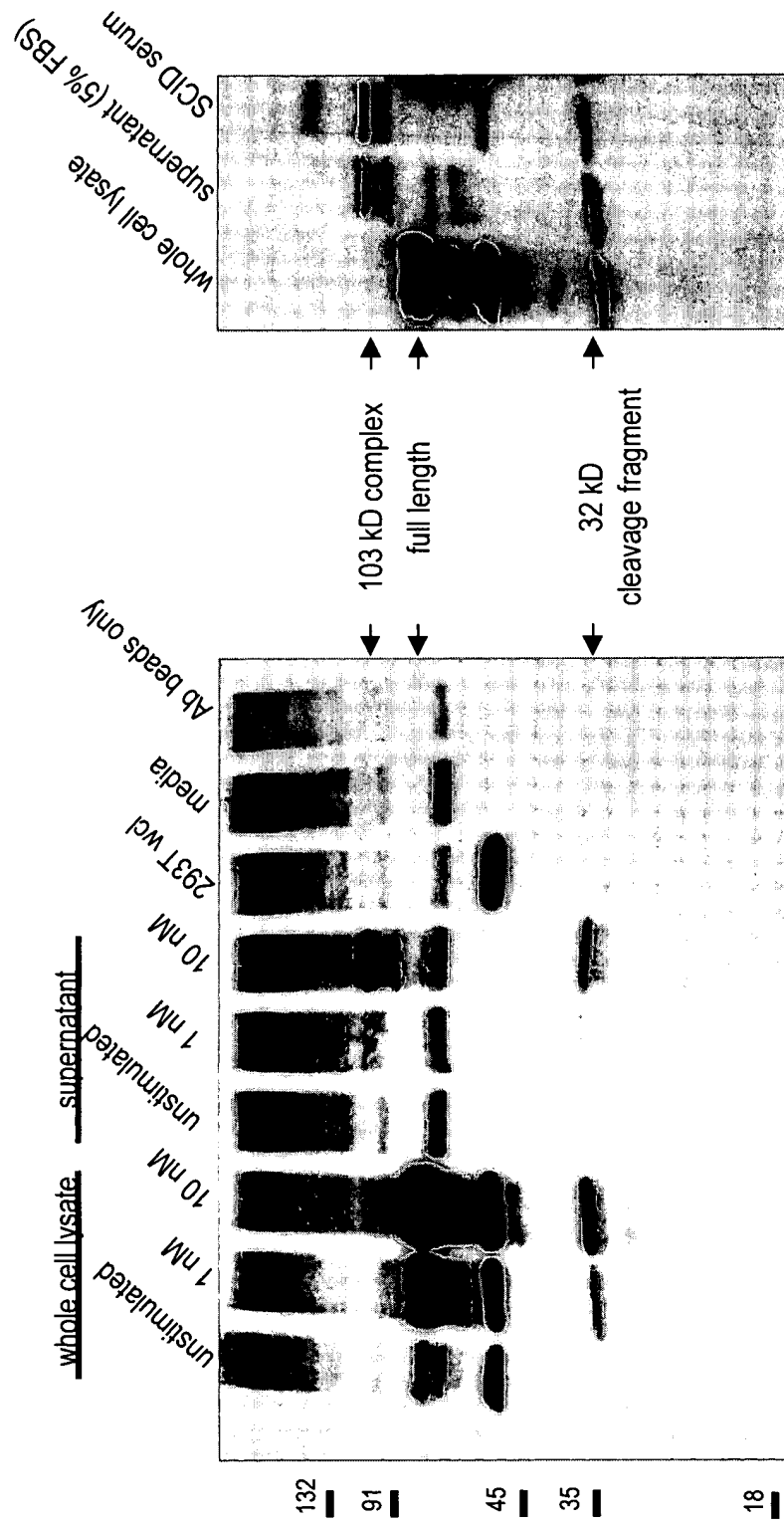


FIG 23

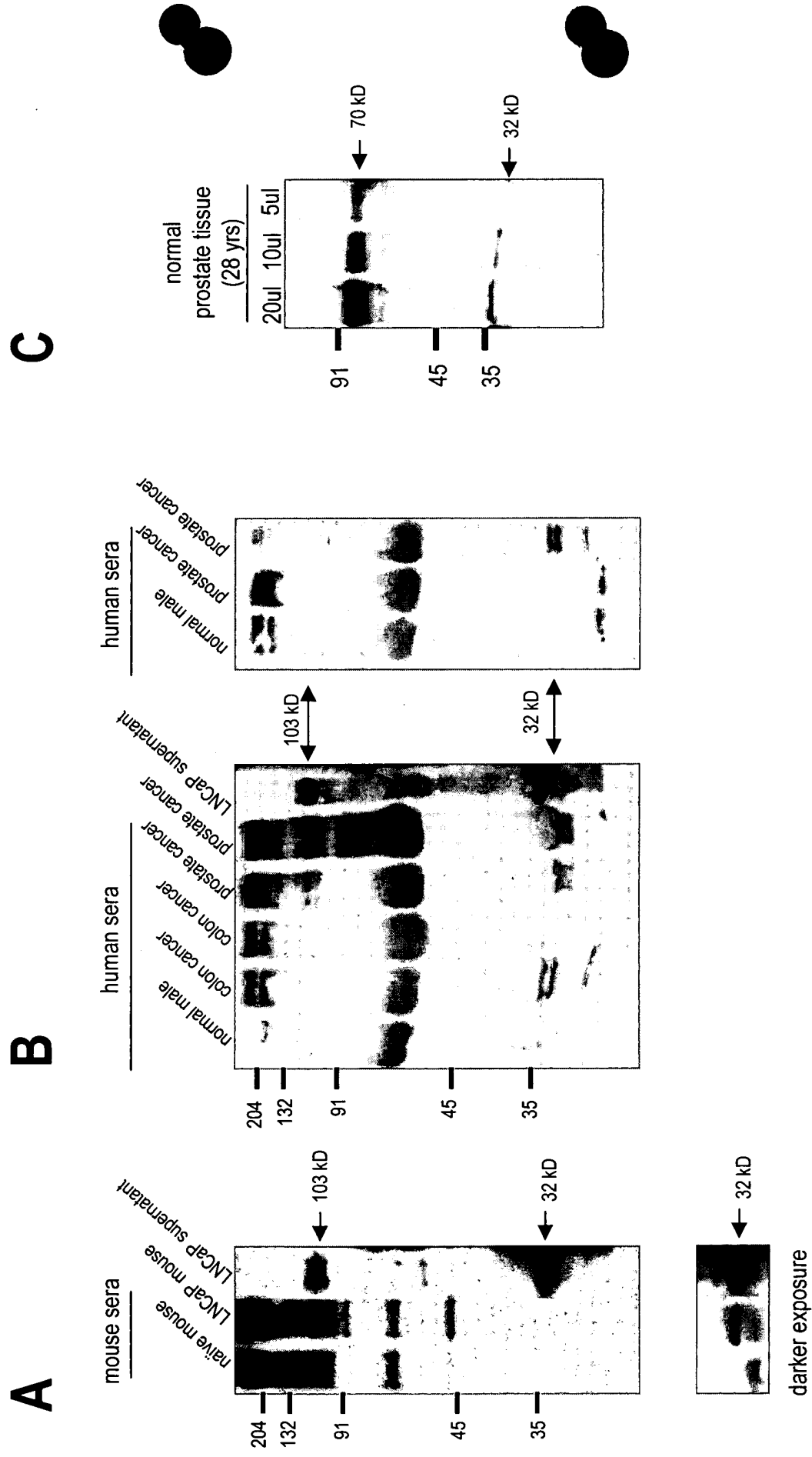
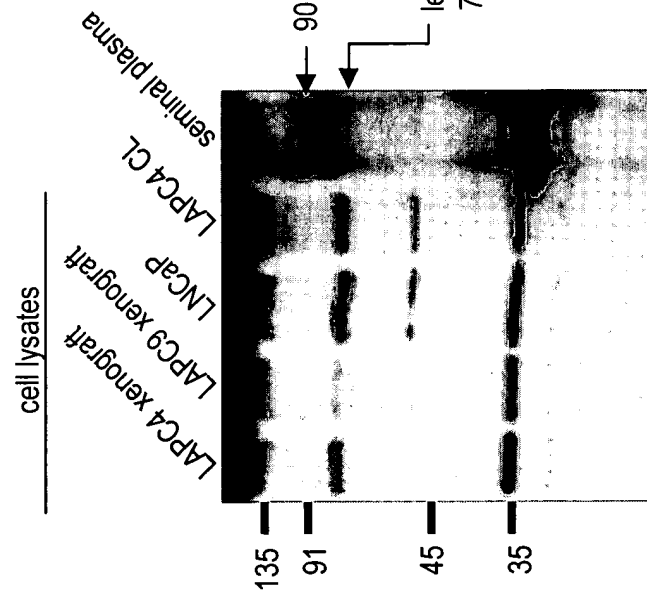


FIG 24

A



B

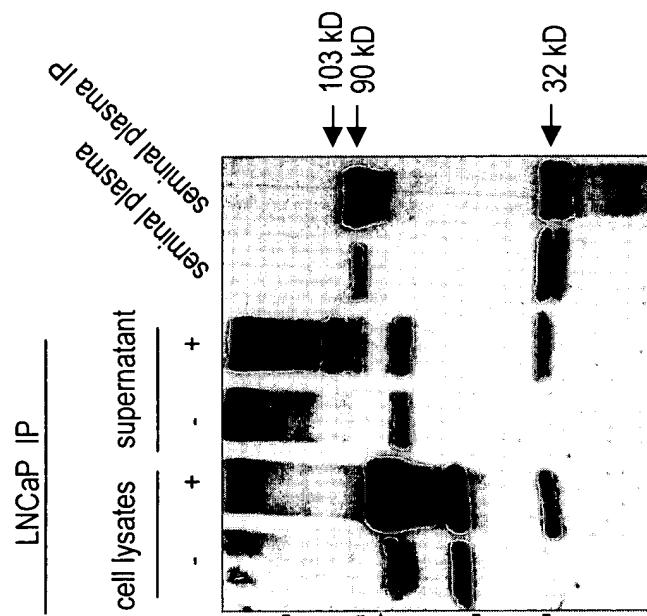


FIG 25

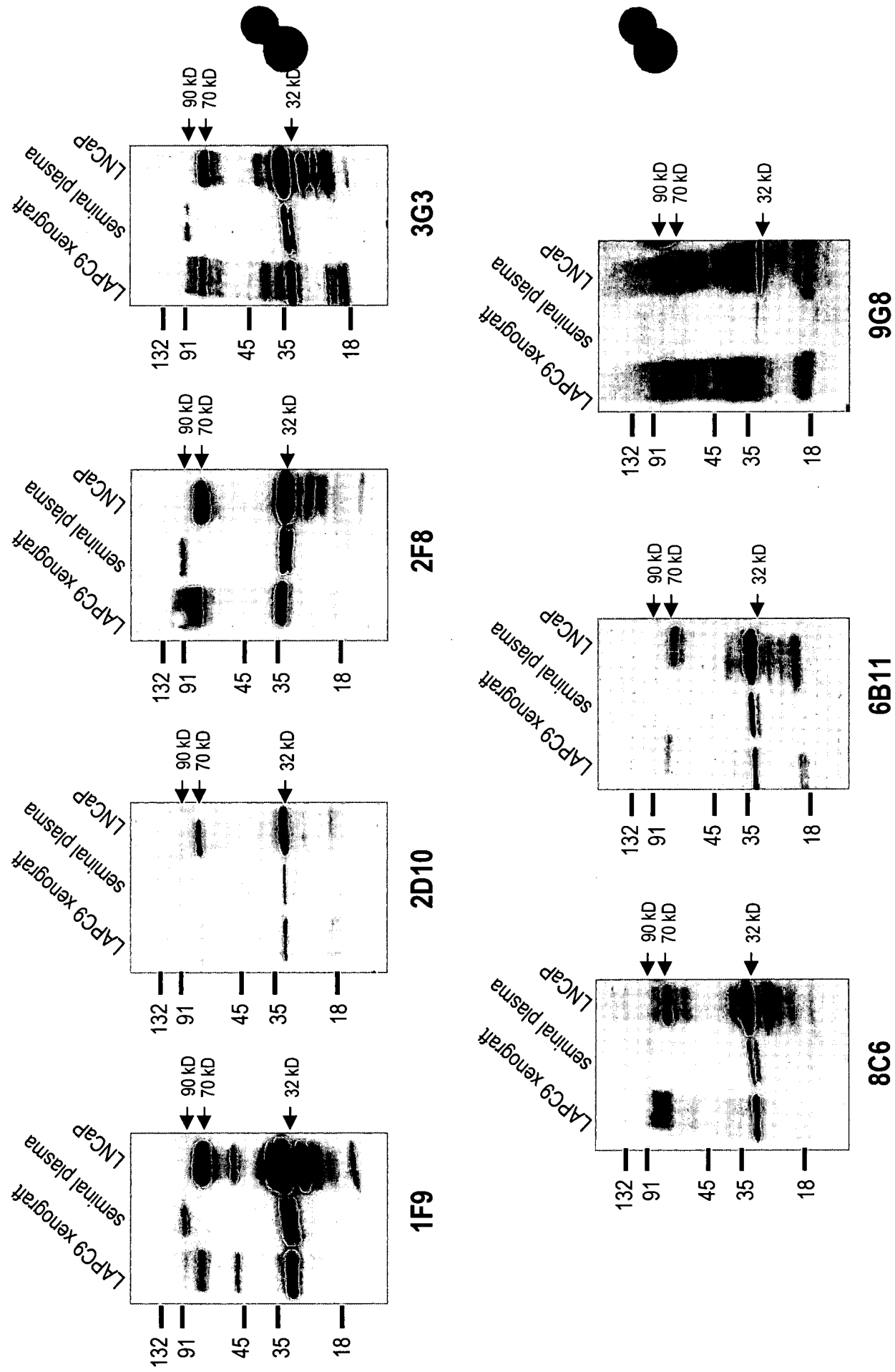


FIG 26

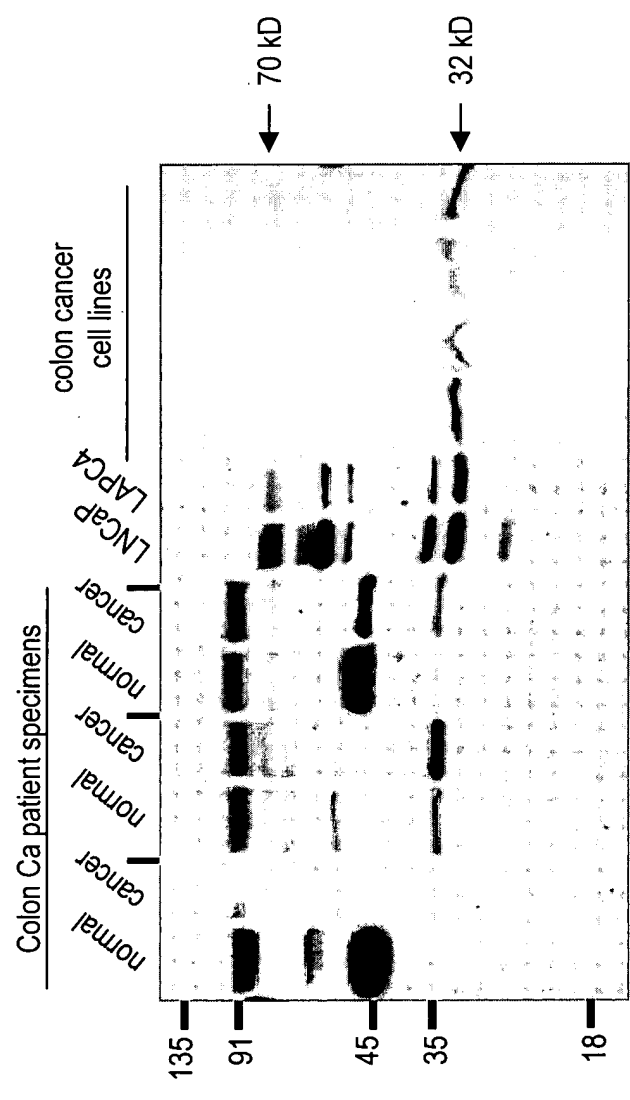


FIG 27A

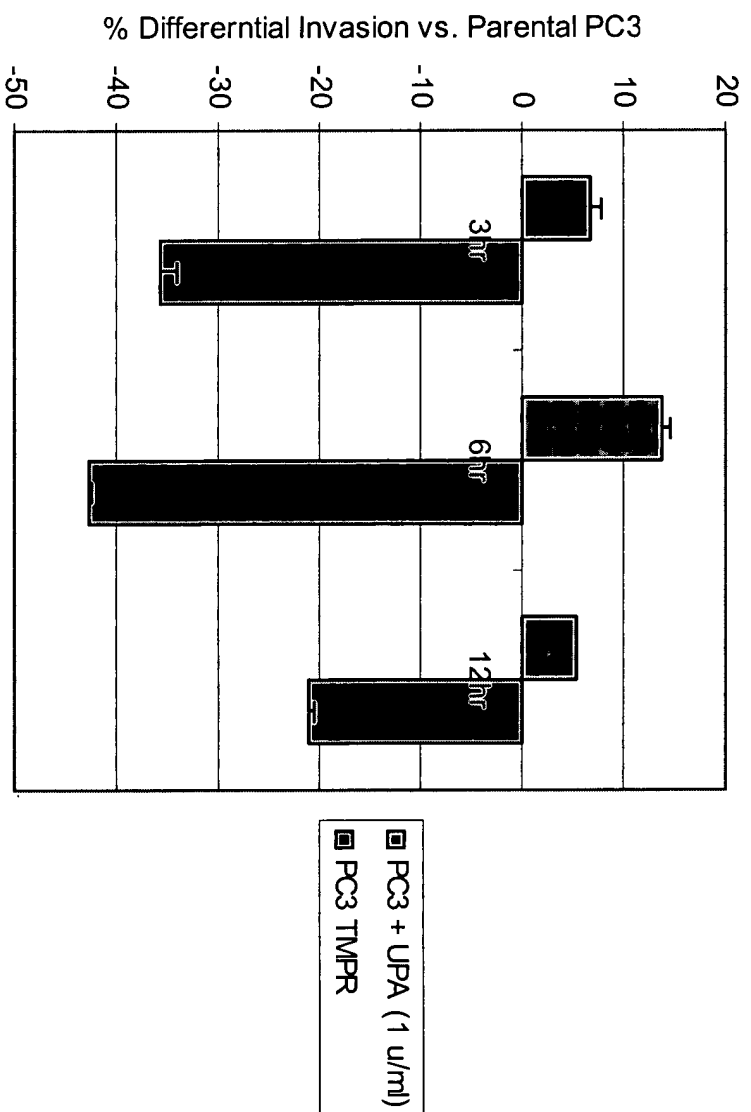


FIG 27B

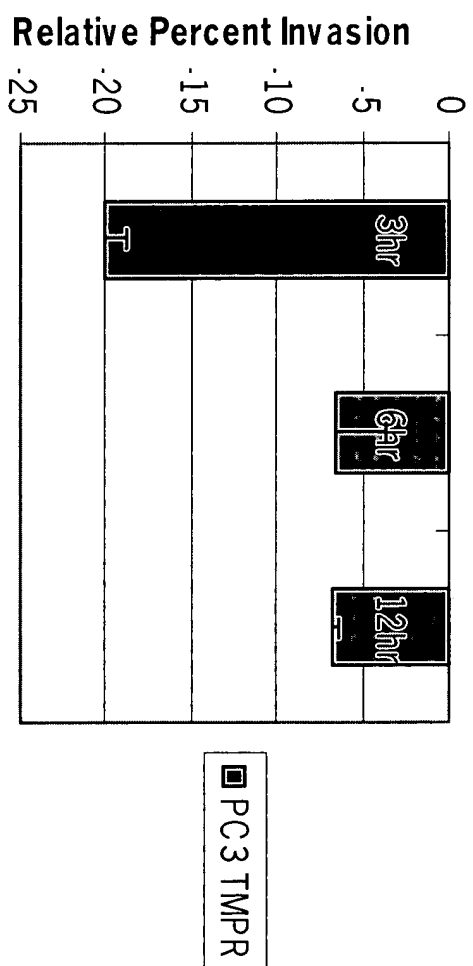


FIG 27C

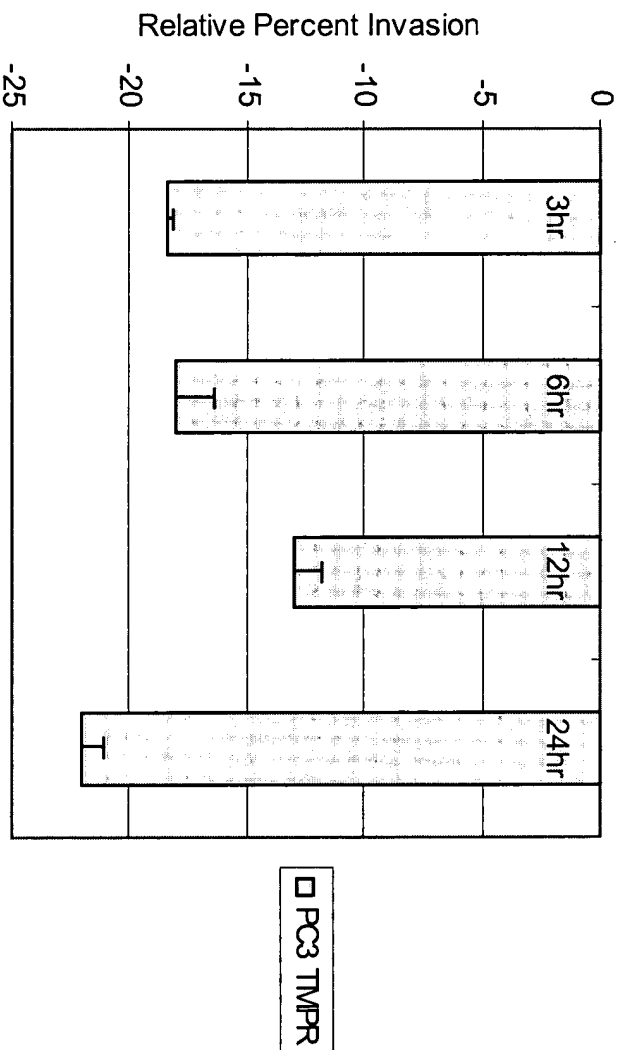


FIG 28

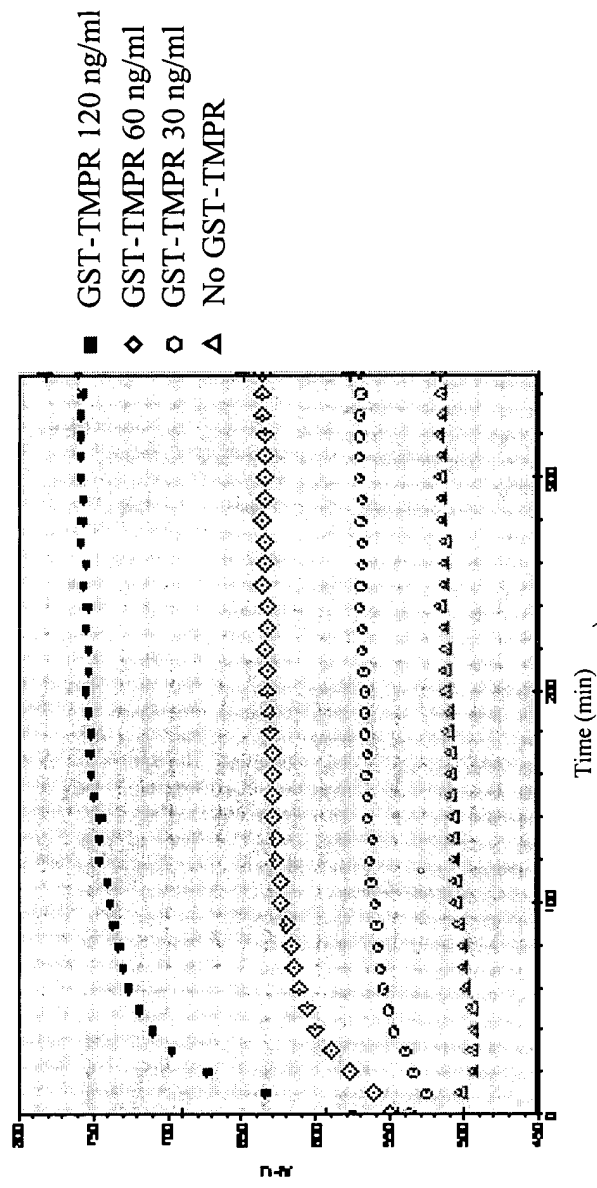


FIG 29

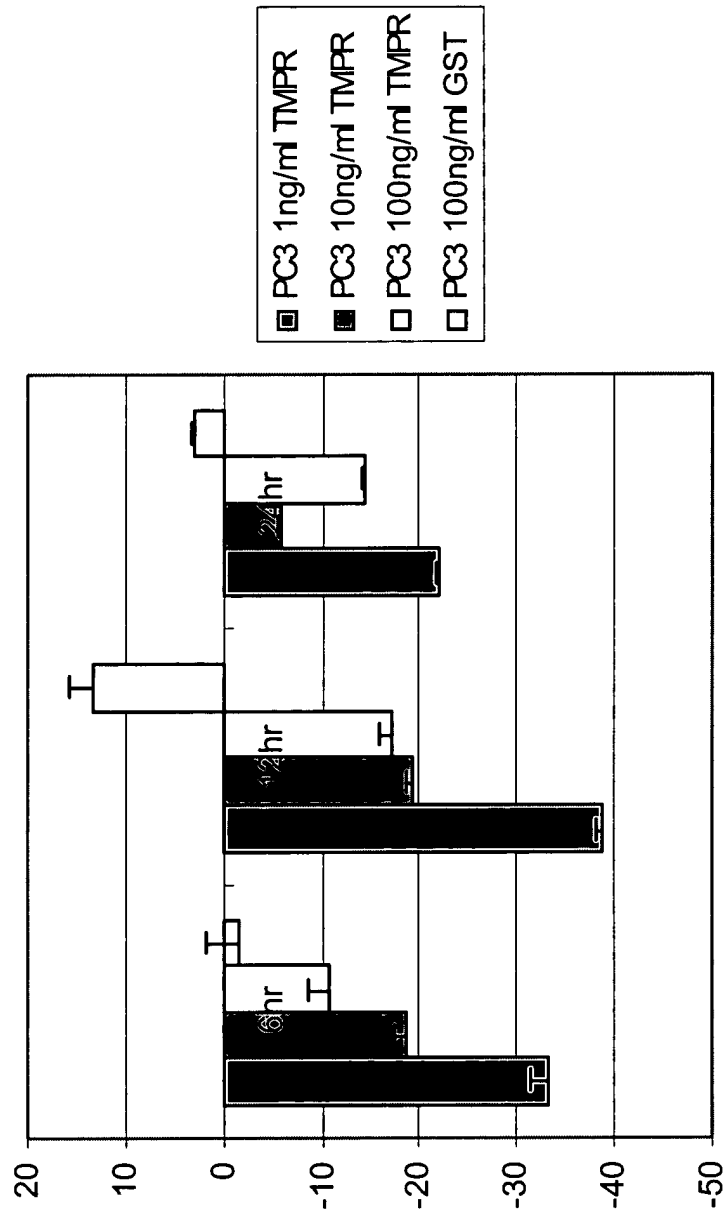


FIG 30

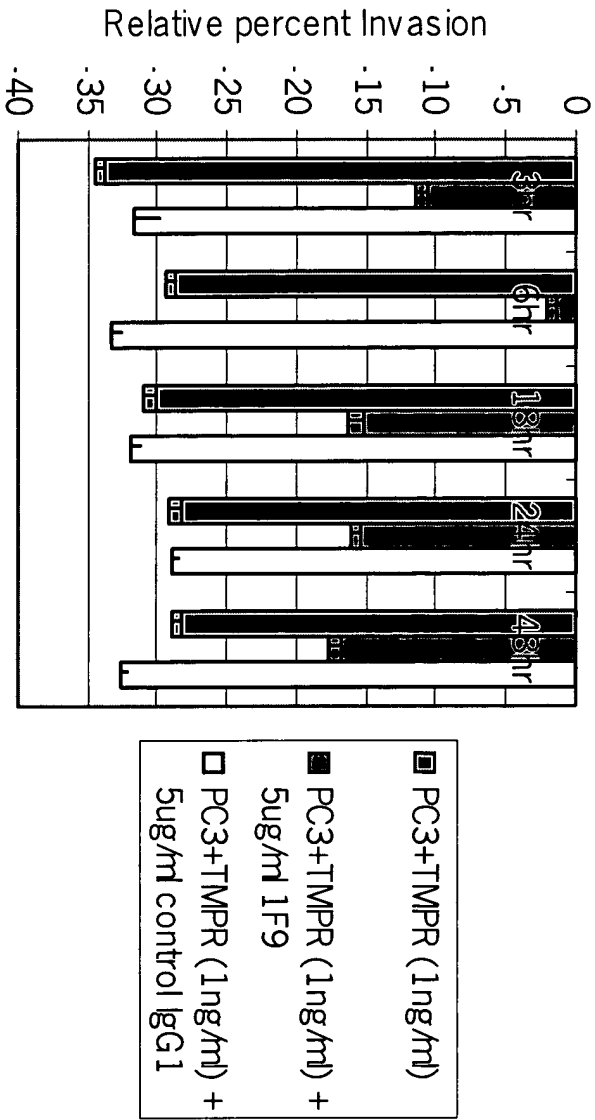
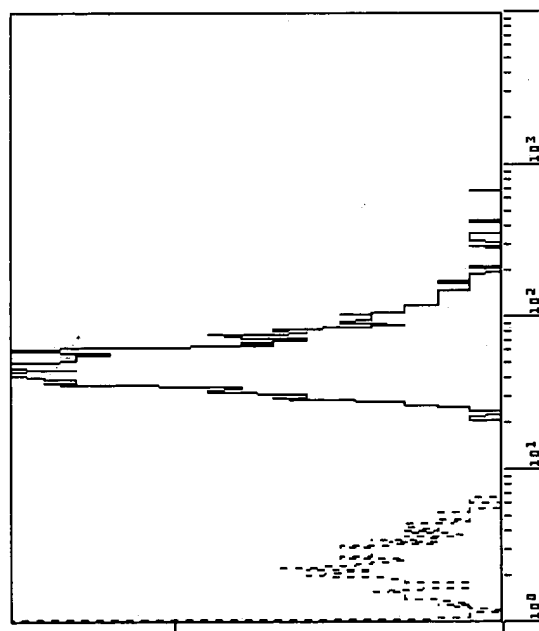


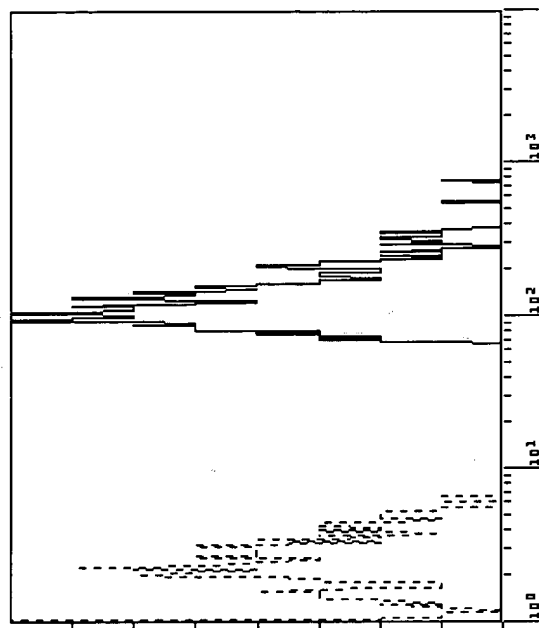
FIG 31

(1):01IC1003.1M0 F11 LOC A



F11 LOC 10uM Morpholino

(1):01IC1006.1M0 F11 LOC A



F11 LOC 30uM Morpholino

FIG 32

